⁂ Reviewed, UniProtKB/Swiss-Prot **P35327** (LUXS_VIBF1)

Last modified December 15, 2009. Version 63.

Names and origin

Protein names	*Recommended name:* **Transcriptional activator protein luxR**
Gene names	Name: **luxR** Ordered Locus Names: VF_A0925
Organism	**Vibrio fischeri (strain ATCC 700601 / ES114)** [Complete proteome] [HAMAP]
Taxonomic identifier	312309 [NCBI]
Taxonomic lineage	Bacteria › Proteobacteria › Gammaproteobacteria › Vibrionales › Vibrionaceae › Aliivibrio

Protein attributes

Sequence length	250 AA.
Sequence status	Complete.
Sequence processing	The displayed sequence is not processed.
Protein existence	Inferred from homology.

General annotation (Comments)

Function	Transcriptional activator of the bioluminescence operon. Binds to the OHHL autoinducer.
Sequence similarities	Belongs to the autoinducer-regulated transcriptional regulatory protein family. Contains 1 HTH luxR-type DNA-binding domain.

Ontologies

Keywords

Biological process	Luminescence Quorum sensing Transcription Transcription regulation

Ligand	DNA-binding
Molecular function	Activator
Technical term	Complete proteome

Gene Ontology (GO)

Biological process	bioluminescence
	Inferred from electronic annotation. Source: UniProtKB-KW
	quorum sensing
	Inferred from electronic annotation. Source: UniProtKB-KW
	regulation of transcription, DNA-dependent
	Inferred from electronic annotation. Source: InterPro
	transcription
	Inferred from electronic annotation. Source: UniProtKB-KW
	two-component signal transduction system (phosphorelay)
	Inferred from electronic annotation. Source: InterPro
Cellular component	intracellular
	Inferred from electronic annotation. Source: InterPro
Molecular function	sequence-specific DNA binding
	Inferred from electronic annotation. Source: InterPro
	transcription factor activity
	Inferred from electronic annotation. Source: InterPro
	two-component response regulator activity
	Inferred from electronic annotation. Source: InterPro

Complete GO annotation...

Sequence annotation (Features)

	Feature key	Position (s)	Length	Description	Graphical view	
Molecule processing						
☐	Chain	1 – 250	250	Transcriptional activator protein luxR		I
Regions						
☐	Domain	176 – 241	66	HTH luxR-type	I I	

☐	DNA binding	200 – 219	20	H-T-H motif Potential	I I
▨	Compositional bias	11 – 20	10	Arg/Lys-rich (basic)	II
▨	Compositional bias	64 – 67	4	Arg/Lys-rich (basic)	II
☐	Compositional bias	104 – 114	11	Lys-rich (basic)	II

Sequences

Sequence		Length	Mass (Da)
P35327-1 [UniParc].			
☐ Last modified February 1, 1994. Version 1. Checksum: 42AC06375E28A34F	FASTA	250	28,520

```
        10         20         30         40         50         60
MNIKNINANE KIIDKIKTCN NNKDINQCLS EIAKIIHCEY YLFAIIYPHS IIKPDVSIID

        70         80         90        100        110        120
NYPEKWRKYY DDAGLLEYDP VVDYSKSHHS PINWNVFEKK TIKKESPNVI KEAQESGLIT

       130        140        150        160        170        180
GFSFPIHTAS NGFGMLSFAH SDKDIYTDSL FLHASTNVPL MLPSLVDNYQ KINTTRKKSD

       190        200        210        220        230        240
SILTKREKEC LAWASEGKST WDISKILGCS ERTVTFHLTN TQMKLNTTNR CQSISKAILT

       250
GAINCPYLKN
```

« Hide

References

« Hide 'large scale' references

[1] **"Sequencing and analysis of luxR and luxI, the luminescence regulatory genes from the squid light organ symbiont Vibrio fischeri ES114."**
Gray K.M., Greenberg E.P.
Mol. Mar. Biol. Biotechnol. 1:414-419(1992)
Cited for: NUCLEOTIDE SEQUENCE [GENOMIC DNA].

"Complete genome sequence of Vibrio fischeri: a symbiotic bacterium with

pathogenic congeners."
Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R., Lostroh
P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E., Stevens A., Visick K.,
[2] Whistler C., Greenberg E.P.
Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005) [PubMed: 15703294]
[Abstract]
Cited for: NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Cross-references

Sequence databases

EMBL ▾	M96844 Genomic DNA. Translation: AAA27542.1. CP000021 Genomic DNA. Translation: AAW87995.1.
RefSeq	YP_206883.1.

3D structure databases

ModBase	Search...

Protein-protein interaction databases

STRING	P35327.

Genome annotation databases

GeneID	3280300.
GenomeReviews	Gene locus VF_A0925 in contig CP000021_GR.
KEGG	vfi:VF_A0925.
NMPDR	fig|312309.3.peg.3316.

Organism-specific databases

CMR	Search...

Phylogenomic databases

HOGENOM	HBG303913.
OMA	ITIRERE.

Enzyme and pathway databases

BioCyc	VFIS312309:VFA0925-MON.

Family and domain databases

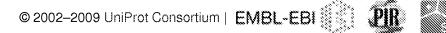| InterPro	IPR005143. Autoind_bd.

	IPR016032. Sig_transdc_resp-reg_C-effctor. IPR000792. Tscrpt_reg_LuxR_C. IPR011991. Wing_hlx_DNA_bd. [Graphical view]
Gene3D	G3DSA:1.10.10.10. Wing_hlx_DNA_bd. 1 hit.
Pfam	PF03472. Autoind_bind. 1 hit. PF00196. GerE. 1 hit. [Graphical view]
PRINTS	PR00038. HTHLUXR.
SMART	SM00421. HTH_LUXR. 1 hit. [Graphical view]
PROSITE	PS00622. HTH_LUXR_1. 1 hit. PS50043. HTH_LUXR_2. 1 hit. [Graphical view]
ProtoNet	Search...

Entry information

Entry name	LUXS_VIBF1
Accession	Primary (citable) accession number: **P35327** Secondary accession number(s): Q5DZ01
Entry history	Integrated into UniProtKB/Swiss-February 1, 1994 Prot: Last sequence update: February 1, 1994 Last modified: December 15, 2009 This is version 63 of the entry and version 1 of the sequence. [Complete history]
Entry status	Reviewed (UniProtKB/Swiss-Prot)
Annotation project	HAMAP (High-quality Automated and Manual Annotation of microbial Proteomes)

Relevant documents

SIMILARITY comments
Index of protein domains and families